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Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

AAN54413 vs SEQ ID NO:4

Sequence 1: aan54413, (226 residues)

Sequence 2: seq (226 residues) SEQ ID NO:4

using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

 Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

85.4% identity in 226 residues overlap; Score: 1012.0; Gap frequency: 0.0%

```
aan54413,      1  MEPIKNLPRLCRTLGYEFKNLDLLTQALTHRSAANKHNERLEFLGDSILSIVISDALYHQ
seq            1  MEPIKNLPRLCRTLGYEFNNIELLIQALTHRSAANKHNERLEFLGDSILSIAISDALYHQ
                ***** *  ** *****

aan54413,     61  FPKATEGDLSRMRATLVRGDTLTLIAQAFKLGDYFLGPGELKSGGFRRESILADAVEAI
seq           61  FPKATEGDLSRMRATLVKGDTLTIIAKEFKLGDYLYLGPGEKSGGFRRESILADAVEAI
                ***** ** *****

aan54413,    121  IGAIYLDSDLEVCRQLLLNWYAERLAEIQPGINQKDAKTLLQEYLGGLKKPLPDYQVINI
seq          121  IGAVYLDADIEVCRKLLLSWYQERLAEIKPGINQKDPKTILQEYLGQFKKPLPDYQVVAV
                ***  *** *  ***  *** ** *****

aan54413,    181  EGD AHDQTFTVECRIDDL SQSVIGVASSRRKAEQIAAAQVLELLKK
seq          181  EGE AHDQTFTVECKISELDKVVTGVASSRRKAEQLAAAQVLELLNK
                ** ***** *  *  *****
```